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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=2; day=12; hr=10; min=20; sec=51; ms=504;]

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Application No: 10521518 Version No: 3.0

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Finished: 2009-01-26 15:40:55.546
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Total Errors: 8
No. of SeqIDs Defined: 110
Actual SeqID Count: 110

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<120> Modulating developmental pathways in plants

<130> 294-208 PCT/US

<140> 10521518

<141> 2006-02-28

<150> PCT/NL03/00524

<151> 2003-07-17

<150> EP 02077908.8

<151> 2002-07-17

<160> 110

<170> PatentIn version 3.2

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35 40 45

Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg
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Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe
65 70 75 80

Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr
85 90 95

Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg
100 105 110

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115 120 125

Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro
130 135 140

Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg
145 150 155 160

Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys
165 170 175

Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg
180 185 190

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35 40 45

Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala
50 55 60

Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu
65 70 75 80

Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu
85 90 95

Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp
100 105 110

Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr
115 120 125

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165 170 175

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180 185 190

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195 200 205

Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro
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260 265 270

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290 295 300

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305 310 315 320

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325 330 335

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340 345 350

Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr
355 360 365

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aaaatcacta ctcaagaaat atg aag aag atg aat gtg gtg gct ttt gtt acg Met Lys Lys Met Asn Val Val Ala Phe Val Thr	533
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45 50 55	
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65 70 75	
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80 85 90	

acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca	1107		
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Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys		
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Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala			
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Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly Thr Ser		
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acacacacacac cttctataaa tagctgacaa aactgattgt tacacacacaac acattcataa 360

atctctcaaa qtaaqaacta aqagctttac tacagtctta ctctctacac attttcttc 420

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tcactttcgt ttgtctcact atg tca aaa gaa gct gag tac cat cca gaa agt 533
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ttgccttcc ctttctatTTt attgtataa atctaatacc cgcgTTaaaaa tttgttttga 653

aattaaacag tat gga cca gga agt ctg aaa tca tac c gtaagtaaaa 701
Tyr Gly Pro Gly Ser Leu Lys Ser Tyr

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Lys	Tyr	His	Lys	Pro	Cys	Met	Phe	Phe	Cys	Gln	Lys	Cys	Cys	Ala	Lys	
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tgc	ctt	tgt	gtc	cct	cca	ggc	acg	tac	ggc	aac	aaa	caa	gtg	tgt	cct	905
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				20					30						

Thr	Lys	Tyr	His	Lys	Pro	Cys	Met	Phe	Phe	Cys	Gln	Lys	Cys	Cys	Ala
					35			40		45					

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atcaaatatct attgcaaaaa atatttataa gaatacaaat gaaaaatgtat aaaatacaaa 180

tgatttctca attacctaaa aaatataaaaa atgtcttact ttattttcag ccactgttgg 240

aaagtacttg caatcatatc gtattttgaa ttataaaaact cagaaacaat tattttccct 300

gaaaagttaa aacttttaat aagatattta taaaataaaaa agaatagtct agaccgaaaa 360

tggggtcgggt tgtccatcca aaggagtgtct ataaatagaa ccctccaagt tctcattagg 420

acacaacaac taaaaccaca tttatcatta cagtctgatt ttagctaaat tctctcatca 480

taaactctcc ttggagaatc atg gct att tca aaa gct ctt atc gct tct ctt 533
 Met Ala Ile Ser Lys Ala Leu Ile Ala Ser Leu
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ctc ata tct ctt gtt ctc caa ctc gtc cag gctgatgtcg tacgtctttt 586
 Leu Ile Ser Leu Leu Val Leu Gln Leu Val Gln

15 20

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tgttacaaca atattcttgc ag gaa aac tca cag aag aaa aat ggt tac gca 698
 Glu Asn Ser Gln Lys Lys Asn Gly Tyr Ala

25

30

aag aag atc g gtaattata tattttttttaaaatccaaacg ttaaaatttag 748
Lys Lys Ile
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agtgagatta ataatctgtg ttttcttcc ttgtatata ag at tgt ggg agt 801
Asp Cys Gly Ser

gcg tgt gta gca cggtgc agg ctt tcg agg agg ccg agg ctg tgt cac 849
Ala Cys Val Ala Arg Cys Arg Leu Ser Arg Arg Pro Arg Leu Cys His
40 45 50 55

aga gcg tgc ggg act tgc tgc tac agg tgc aac tgt gtg cct ccg ggt 897